

A. Harris

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/397,558

DATE: 10/21/1999
TIME: 09:32:35

INPUT SET: S33714.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#7

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Lal, Preeti
Guegler, Karl J.
Corley, Neil C.

ENTERED

(ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 PORTER DRIVE
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/397,558
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/083,521
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CERRONE, MICHAEL C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0527 US

(ix) TELECOMMUNICATION INFORMATION:

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47 (A) TELEPHONE: (650) 855-0555
48 (B) TELEFAX: (650) 845-4166
49
50
51

52 (2) INFORMATION FOR SEQ ID NO: 1:
53

54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 141 amino acids
56 (B) TYPE: amino acid
57 (C) STRANDEDNESS: single
58 (D) TOPOLOGY: linear
59

60 (vii) IMMEDIATE SOURCE:
61 (A) LIBRARY: PROSTUT10
62 (B) CLONE: 1691243
63

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :
65

66	Met	Val	His	Val	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	
67				5						10					15	
68	Glu	Arg	Tyr	Leu	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	
69				20						25					30	
70	Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	Val	Trp	Arg	Ile	Glu	
71				35						40					45	
72	Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	Ser	Leu	
73				50						55					60	
74	Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	
75				65						70					75	
76	Arg	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	
77				80						85					90	
78	Leu	Ile	Ser	Thr	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	
79				95						100					105	
80	Phe	Glu	Glu	Glu	Tyr	Tyr	Arg	Phe	Tyr	Thr	Pro	Pro	Asn	Phe	Val	
81				110						115					120	
82	Leu	Ala	Leu	Val	Leu	Pro	Ser	Ile	Val	Ile	Leu	Asp	Leu	Leu	Gln	
83				125						130					135	
84	Leu	Cys	Arg	Tyr	Pro	Asp										
85				140												
86																
87																
88																
89																

90 (2) INFORMATION FOR SEQ ID NO: 2:
91

92 (i) SEQUENCE CHARACTERISTICS:
93 (A) LENGTH: 410 amino acids
94 (B) TYPE: amino acid
95 (C) STRANDEDNESS: single
96 (D) TOPOLOGY: linear
97

98 (vii) IMMEDIATE SOURCE:
99 (A) LIBRARY: BRSTTUT03

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100          (B) CLONE: 1999442
101
102          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :
103
104  Met  Phe  Leu  Pro  Pro  Val  Val  Leu  Ala  Ile  Arg  Ser  Arg  Tyr  Val
105                      5          10          15
106  Leu  Glu  Ala  Ala  Val  Tyr  Thr  Phe  Thr  Met  Phe  Phe  Ser  Thr  Phe
107                      20          25          30
108  Tyr  His  Ala  Cys  Asp  Gln  Pro  Gly  Ile  Val  Val  Phe  Cys  Ile  Met
109                      35          40          45
110  Asp  Tyr  Asp  Val  Leu  Gln  Phe  Cys  Asp  Phe  Leu  Gly  Ser  Leu  Met
111                      50          55          60
112  Ser  Val  Trp  Val  Thr  Val  Ile  Ala  Met  Ala  Arg  Leu  Gln  Pro  Val
113                      65          70          75
114  Val  Lys  Gln  Val  Leu  Tyr  Leu  Leu  Gly  Ala  Met  Leu  Leu  Ser  Met
115                      80          85          90
116  Ala  Leu  Gln  Leu  Asp  Arg  His  Gly  Leu  Trp  Asn  Leu  Leu  Gly  Pro
117                      95          100         105
118  Ser  Leu  Phe  Ala  Leu  Gly  Ile  Leu  Ala  Thr  Ala  Trp  Thr  Val  Arg
119                      110         115         120
120  Ser  Val  Arg  Arg  Arg  His  Cys  Tyr  Pro  Pro  Thr  Trp  Arg  Arg  Trp
121                      125         130         135
122  Leu  Phe  Tyr  Leu  Cys  Pro  Gly  Ser  Leu  Ile  Ala  Gly  Ser  Ala  Val
123                      140         145         150
124  Leu  Leu  Tyr  Ala  Phe  Val  Glu  Thr  Arg  Asp  Asn  Tyr  Phe  Tyr  Ile
125                      155         160         165
126  His  Ser  Ile  Trp  His  Met  Leu  Ile  Ala  Gly  Ser  Val  Gly  Phe  Leu
127                      170         175         180
128  Leu  Pro  Pro  Arg  Ala  Lys  Thr  Asp  His  Gly  Val  Pro  Ser  Gly  Ala
129                      185         190         195
130  Arg  Ala  Arg  Gly  Cys  Gly  Tyr  Gln  Leu  Cys  Ile  Asn  Glu  Gln  Glu
131                      200         205         210
132  Glu  Pro  Gly  Pro  Arg  Gly  Pro  Arg  Arg  Gly  His  Cys  Gln  Gln  His
133                      215         220         225
134  Leu  Cys  Gln  Leu  Arg  Gly  Ala  Leu  Gly  Leu  Ala  Leu  Arg  Gly  Tyr
135                      230         235         240
136  Glu  Cys  Phe  Leu  Glu  Phe  Phe  Leu  Gly  Val  Trp  Ser  Pro  Leu  Arg
137                      245         250         255
138  Arg  Arg  Gln  Ala  Val  Phe  Leu  Glu  Asp  Met  Glu  Ser  Phe  Ser  Arg
139                      260         265         270
140  Thr  Gln  Asn  Ser  Ser  Arg  Asp  Leu  Glu  Pro  Phe  Pro  Gly  His  Gly
141                      275         280         285
142  Glu  Leu  Pro  Glu  Gly  Leu  Glu  Ser  Pro  Cys  Ile  Met  Glu  Ser  Phe
143                      290         295         300
144  Leu  Arg  Thr  Gly  Ala  Tyr  Ala  Gly  Thr  Glu  Ser  Leu  Arg  Thr  Lys
145                      305         310         315
146  Glu  Ser  Leu  Leu  Gln  Val  Trp  Ser  Leu  Ser  Trp  Asp  Ala  Glu  Pro
147                      320         325         330
148  Ser  Gln  Asp  Met  Asp  Ser  Phe  Pro  Gly  Arg  Gln  Ser  Pro  Val  Arg
149                      335         340         345
150  Ser  Thr  Ala  Ser  Phe  Gln  Arg  Arg  Trp  Ser  Leu  Ser  Trp  Gly  Asn
151                      350         355         360
152  Gln  Ile  Ser  Arg  Phe  Ser  Gln  Arg  Leu  Ser  Asn  Ser  Gly  Leu  Arg

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153		365		370		375
154	Leu Pro Ser Gln Arg Gln Arg Leu Gly Cys Ala Val Leu Trp Arg					
155		380		385		390
156	Arg Asp Cys Arg Met Asp Gly Ala Gly Thr Gly Ala Val Trp Val					
157		395		400		405
158	Ala Gly Ile Leu Val					
159		410				

160

161

162

163

164 (2) INFORMATION FOR SEQ ID NO: 3:

165

166 (i) SEQUENCE CHARACTERISTICS:

167 (A) LENGTH: 1213 base pairs

168 (B) TYPE: nucleic acid

169 (C) STRANDEDNESS: single

170 (D) TOPOLOGY: linear

171

172 (vii) IMMEDIATE SOURCE:

173 (A) LIBRARY: PROSTUT10

174 (B) CLONE: 1691243

175

176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

177

178	CAAGTATAGG	AGATTTCCAC	CTTG GTT GGA	AACCTGGTTA	CAGTGTAGAA	AACAGCTTGG	60
179	ATTACTAAGT	TTTTTCTTCG	CTATGGTCCA	TGTTGCCTAC	AGCCTCTGCT	TACCGATGAG	120
180	AAGGTCAGAG	AGATATTTGT	TTCTCAACAT	GGCTTATCAG	CAGGTTCATG	CAAATATTGA	180
181	AAACTCTTGG	AATGAGGAAG	AAGTTTGGAG	AATTGAAATG	TATATCTCCT	TTGGCATAAT	240
182	GAGCCTTGGC	TTACTTTCCC	TCCTGGCAGT	CACCTCTATC	CCTTCAGTGA	GCAATGCCTT	300
183	AAACTGGAGA	GAATTCAGTT	TTATTCAGTC	TACACTTGGA	TATGTCGCTC	TGCTCATAAG	360
184	TACTTTCCAT	GTTTTAATTT	ATGGATGGAA	ACGAGCTTTT	GAGGAAGAGT	ACTACAGATT	420
185	TTATACACCA	CCAACTTTG	TTCTTGCTCT	TGTTTTGCCC	TCAATTGTAA	TTCTGGATCT	480
186	TTTGCAGCTT	TGCAGATACC	CAGACTGAGC	TGGAAGTGG	ATTTGTCTTC	CTATTGACTC	540
187	TACTTCTTTA	AAAGCGGCTG	CCCATTACAT	TCCTCAGCTG	TCCTTGCACT	TAGGTGTACA	600
188	TGTGACTGAG	TGTTGGCCAG	TGAGATGAAG	TCTCCTCAA	GGAAGGCAGC	ATGTGTCTCT	660
189	TTTCATCCCT	TCATCTTGCT	GCTGGGATTG	TGGATATAAC	AGGAGCCCTG	GCAGCTGTCT	720
190	CCAGAGGATC	AAAGCCACAC	CCAAAGAGTA	AGGCAGATTA	GAGACCAGAA	AGACCTTGAC	780
191	TACTTCCCTA	CTTCCACTGC	TTTTTCCTGC	ATTTAAGCCA	TTGTAAATCT	GGGTGTGTTA	840
192	CATGAAGTGA	AAATTAATTC	TTTCTGCCCT	TCAGTTCTTT	ATCCTGATAC	CATTTAACAC	900
193	TGTCTGAATT	AACTAGACTG	CAATAATTCT	TTCTTTTGAA	AGCTTTTAAA	GGATAATGTG	960
194	CAATTCACAT	TAAAATTGAT	TTTCCATTGT	CAATTAGTTA	TACTCATTTT	CCTGCCTTGA	1020
195	TCTTTCATTA	GATATTTTGT	ATCTGCTTGG	AATATATTAT	CTTCTTTTAA	ACTGTGTAAT	1080
196	TGGTAATTAC	TAAAACCTCTG	TAATCTCCAA	AATATTGCTA	TCAAATTACA	CACCATGTTT	1140
197	TCTATCATTC	TCATAGATCT	GCCTTATAAA	CATTTAAATA	AAAAGTACTA	TTTAATGATT	1200
198	TAAAAAAA	AAA					1213

199

200

201 (2) INFORMATION FOR SEQ ID NO: 4:

202

203 (i) SEQUENCE CHARACTERISTICS:

204 (A) LENGTH: 1297 base pairs

205 (B) TYPE: nucleic acid

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206 (C) STRANDEDNESS: single
207 (D) TOPOLOGY: linear
208
209 (vii) IMMEDIATE SOURCE:
210 (A) LIBRARY: BRSTTUT03
211 (B) CLONE: 1999442
212
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
214
215 CGGACGCGTG GGCTGCTCTG CCTGAGCAAC CTCATGTTTC TGCCACCTGT GGTCTGGCC 60
216 ATTCGGAGTC GATATGTGCT GGAAGCTGCA GTCTACACCT TCACCATGTT CTTCTCCACG 120
217 TTCTATCATG CCTGTGACCA GCCAGGCATC GTGGTTTTCT GCATCATGGA CTACGATGTG 180
218 CTGCAGTTCT GTGATTTCTT GGGCTCCTTA ATGTCCGTGT GGGTCACTGT CATTGCCATG 240
219 GCTCGTTTAC AGCCCGTGGT CAAGCAGGTG CTGTATTTGC TGGGAGCTAT GCTGCTGTCC 300
220 ATGGCTCTGC AGCTTGACCG ACATGGACTC TGGAACCTGC TTGGACCCAG TCTCTTCGCC 360
221 CTGGGGATCT TGGCCACAGC CTGGACAGTA CGCAGCGTCC GCCGCCGCA CTGCTACCCA 420
222 CCCACGTGGC GCCGCTGGCT TTTCTACTTG TGCCCTGGCA GCCTTATTGC AGGCAGTGCC 480
223 GTCCTGCTTT ATGCTTTTGT GGAGACCCGG GACAACTACT TCTACATTCA CAGCATTTGG 540
224 CATATGCTCA TTGCGGGCAG TGTGGGCTTC CTGCTGCCCC CTCGTGCCAA GACTGACCAC 600
225 GGGGTCCCAT CTGGAGCCCG GGCCCGGGG TGTTGGTTACC AGCTATGCAT CAACGAGCAG 660
226 GAGGAGCCTG GGCCTCGTGG GCCCAGGAG GGCCACTGTC AGCAGCATCT GTGCCAGCTG 720
227 AGAGGGGCTT TGGGCCCTGGC CCTGAGGGGA TATGAATGCT TCCTAGAGTT CTTTCTGGGG 780
228 GTGTGGAGCC CTCTTAGAAG GAGACAGGCT GTATTTCTTG AGGACATGGA GTCTTTCTCA 840
229 AGGACACAAA ACTCTTCCAG GGACCTGGAG CCCTTCCCAG GACATGGAGA ACTTCTGAG 900
230 GGCTTGGAGT CCCCCTGCAT CATGGAGTCC TTCTTAAGGA CTGGAGCCTA TGCAGGCACA 960
231 GAGTCCCTCA GGACCAAGGA GTCCCTCCTG CAGGTGTGGA GCCTTTCCTG GGATGCAGAG 1020
232 CCTTCCCAAG ACATGGATTC CTTCCCAGGG AGACAAAGCC CTGTCAGGAG CACAGCATCT 1080
233 TTCCAGAGGA GGTGGAGTCT ATCTTGGGGA AACCAAATTT CCAGATTTTC CCAGAGGCTC 1140
234 AGCAACTCTG GCCTCAGGCT TCCTTCCCAG AGGAGCGTCT TGGGCTGTGC TGTGCTGTGG 1200
235 AGGAGGGATT GCAGGATGGA TGGAGCTGGG ACTGGGGCTG TCTGGGTGGC TGGTATCCTC 1260
236 GTTTGATACA GGTGGAGTCT CTGTGCTCTC ATAGAAG 1297

237
238
239 (2) INFORMATION FOR SEQ ID NO: 5:
240

241 (i) SEQUENCE CHARACTERISTICS:
242 (A) LENGTH: 76 amino acids
243 (B) TYPE: amino acid
244 (C) STRANDEDNESS: single
245 (D) TOPOLOGY: linear
246

247 (vii) IMMEDIATE SOURCE:
248 (A) LIBRARY: GenBank
249 (B) CLONE: 1216498
250

251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :
252

253 Met Gly Arg Ala Met Val Val Arg Leu Gly Leu Gly Leu Leu Leu
254 5 10 15
255 Leu Ala Leu Leu Leu Pro Thr Gln Ile Tyr Cys Asn Gln Thr Ser
256 20 25 30
257 Val Ala Pro Phe Ser Gly Asn Gln Ser Ile Ser Ala Ala Pro Asn
258 35 40 45

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SEQUENCE VERIFICATION REPORT
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Error

Original Text

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SEQUENCE MISSING ITEM REPORT
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SEQUENCE CORRECTION REPORT
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Original Text

Corrected Text